

SEQUENCE LISTING

<110> Ni et al.

<120> I-FLICE, A Novel Inhibitor of Tumor Necrosis Factor Receptor-1 and CD-95 Induced Apoptosis

<130> PF381C1D1

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<151> 2000-01-21

<150> US 09/009,893
<151> 1998-01-21

<150> US 60/054,800
<151> 1997-08-05

<150> US 60/034,205
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<170> PatentIn version 3.2

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Cys Leu Ser Gln Lys Leu Arg Gln Glu Arg Lys Arg Pro Leu Leu Asp	
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Lys Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg
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Phe Asp Leu Leu Lys Arg Ile Leu Lys Met Asp Arg Lys Ala Val Glu
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Thr His Leu Leu Arg Asn Pro His Leu Val Ser Asp Tyr Arg Val Leu
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Ile Phe Leu Met Lys Asp Tyr Met Gly Arg Gly Lys Ile Ser Lys Glu
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Gln Glu Arg Lys Arg Pro Leu Leu Asp Leu His Ile Glu Leu Asn Gly
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Ser Lys Cys Lys Leu Asp Asp Asp Met Asn Leu Leu Asp Ile Phe Ile
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Asp Tyr Glu Glu Phe Ser Lys Glu Arg Ser Ser Ser Leu Glu Gly Ser
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Pro Asp Glu Phe Ser Asn Gly Glu Glu Leu Cys Gly Val Met Thr Ile
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Val Tyr Gln Met Lys Ser Lys Pro Arg Gly Tyr Cys Leu Ile Ile Asn
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Asn His Asn Phe Ala Lys Ala Arg Glu Lys Val Pro Lys Leu His Ser
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 Ile Arg Asp Arg Asn Gly Thr His Leu Asp Ala Gly Leu Thr Thr Thr
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 Phe Glu Glu Leu His Phe Glu Ile Lys Pro His Asp Asp Cys Thr Val
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 Pro Val Glu Thr Asp Ser Glu Glu Gln Pro Tyr Leu Glu Met Asp Leu
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 Pro Arg Gly Asp Asp Ile Leu Thr Ile Leu Thr Glu Val Asn Tyr Glu
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 Ile Glu Ala Asp Ala Leu Asn Pro Glu Gln Ala Pro Thr Ser Leu Gln
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 Asp Ser Ile Pro Ala Glu Ala Asp Phe Leu Leu Gly Leu Ala Thr Val
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 Pro Gly Tyr Val Ser Phe Arg His Val Glu Glu Gly Ser Trp Tyr Ile
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 Glu Lys Ser Phe Leu Asp Leu Val Glu Leu Glu Lys Leu Asn Leu
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His	Arg	Ile	Asp	Leu	Lys	Thr	Lys	Ile	Gln	Lys	Tyr	Lys	Gln	Ser	Val		
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Lys Ser Phe Leu Asp Leu Val Val Glu Leu Glu Lys Leu Asn Leu Val
 35 40 45

Ala Pro Asp Gln Leu Asp Leu Leu Glu Lys Cys Leu Lys Asn Ile His
 50 55 60

Arg Ile Asp Leu Lys Thr Lys Ile Gln Lys Tyr Lys Gln Ser Val Gln
 65 70 75 80

Gly Ala Gly Thr Ser Tyr Arg Asn Val Leu Gln Ala Ala Ile Gln Lys
 85 90 95

Ser Leu Lys Asp Pro Ser Asn Asn Phe Arg Glu Glu Pro Val Lys Lys
 100 105 110

Ser Ile Gln Glu Ser Glu Ala Phe Leu Pro Gln Ser Ile Pro Glu Glu
 115 120 125

Arg Tyr Lys Met Lys Ser Lys Pro Leu Gly Ile Cys Leu Ile Ile Asp
 130 135 140

Cys Ile Gly Asn Glu Thr Glu Leu Leu Arg Asp Thr Phe Thr Ser Leu
 145 150 155 160

Gly Tyr Glu Val Gln Lys Phe Leu His Leu Ser Met His Gly Ile Ser
 165 170 175

Gln Ile Leu Gly Gln Phe Ala Cys Met Pro Glu His Arg Asp Tyr Asp
 180 185 190

Ser Phe Val Cys Val Leu Val Ser Arg Gly Gly Ser Gln Ser Val Tyr
 195 200 205

Gly Val Asp Gln Thr His Ser Gly Leu Pro Leu His His Ile Arg Arg

210	215	220
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225	230	235 240
Phe Phe Ile Gln Asn Tyr Val Val Ser Asp Gly Gln Leu Glu Asp Ser		
	245	250 255
Ser Leu Leu Glu Val Asp Gly Pro Ala Met Lys Asn Val Glu Phe Lys		
	260	265 270
Ala Gln Lys Arg Gly Leu Cys Thr Val His Arg Glu Ala Asp Phe Phe		
	275	280 285
Trp Ser Leu Cys Thr Ala Asp Met Ser Leu Leu Glu Gln Ser His Ser		
	290	295 300
Ser Pro Ser Leu Tyr Leu Gln Cys Leu Ser Gln Lys Leu Arg Gln Glu		
305	310	315 320
Arg Gly Thr Ile Pro Gly Ser Gly Ile Thr Glu Ser Lys Asp Met His		
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Phe Ser Ser Leu Gly Cys Ile Leu Leu Asp Val Leu		
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26

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27

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 accttgtttc ggactataga gtgctgatgg cagagattgg tgaggatttg gataaatctg 180
 atgtgtcctc attaatatttc ctcatgaagg attacatggg ccgaggcaag ataagcaagg 240
 agaagagttt cttgggacct tgggtggttga gttgggagaa actaaatctg gtttgcccca 300
 gatcaactng ggatttntta ggaaaaatgc ctaaagaaca tncacaggat agacctgnag 360
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tgggaggcca aggagggcag atcacttcag gtcaggagtt cgagaccagc ctggccaaca 180

tggtaaacgc tgtccctagt aaaantacaa aanttagctg ggtgtgggtg tgggtacctg	240
tgttcccagt tacttgggag gctgaggtgg gaggatcttt tggaaccag gagtttcagg	300
gtcatagcat gctgtgnttg tgccctnacg aattagccac tgcattacca acctggggca	360
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cataagaaac caaaaggctg ggcgtagtgg ctacgcctg tgatcccagc actttgggag	180
gccggggagg gcagatcact tcaggtcagg agttcgagac cggcctggnc aacatggtag	240
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 cagagggcca gctggaggac agcagcctct tggagggtgga tgggccagcn atgaagaatg 180
 tggaattcaa ggctcagaag cgagggctgt gcacagttca ccgagnaagc tgacttcttc 240
 tggagcctgt gtaatgcgga catgtccctg cttggagcaa tcttcanagg ttcancgtcc 300
 ctgtnacctg catgcctttt cccagaaact gngacaagna agaaaacgnc cantnctggg 360
 gntntttcac attggaactc aatggttaca anttatgntt ggggncaaca anttttttgc 420
 caagggggaa ttttttgttt tgggntgnag aaaaatttng ggaaagaant ttttccttn 480
 cnnnaaatta ggnacccaaa 500

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agttgactgc ctgctggctt tctgttgact ggcctggagc tgtactgcaa gacccttggt 180
agcttccta gtctaagagt aggatgtctg ctgaagtcac ccatcagggt gaagaagcac 240
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agaagtaaag aacaaagact taaggaacag cttggcgctc aacaagaacc agtgnaagaa 120

atccattcag gaatcagaag cttttttgcc tcagagcata cctgaagaga gatacaagat 180

gaagagcaag cccctagga atctgcctga taaatcgatt gcattggcaa tgaggacaga 240

gcttcttcgg ggacaccttc acttccctgg gcttatgaag tnccaggaaa ttcttgcac 300

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 agttgnctgc ctgctggctt tctgttgact ggcctggagc tgtactgcaa gacccttgtg 180
 agcttccta gtctaagagt aggatgtctg ctgaagtcac ccatcagggt gaagaagcac 240
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 agttgactgc ctgctggctt tctgttgact ggcctggagc tgtactgcaa gacccttgtg 180
 agcttccta gtctaagagt aggatgtctg ctgaagtcac ccatcagggt gaagaagcac 240
 ttgatacaga tgagaaggag atgctgctct ttttgtgcc gggatgttgc tatagat 297

<210> 31
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<400> 31
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 ctgcatgctc ttatatattcc tcaagttttg acaatttgat aggtgaaaag tggatatctga 120
 ttgttcagat ctggaaggct ttgttatata aacatttttt taatgtttat tggcaagaat 180
 acttttctaa gagaaacatc agtgagctgg tttccattta agctgaatga agccacaatg 240
 tacctcaagt ataaggttaa ctggcctttt ttcagttgca ctctaattac aatttagaat 300
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 ctgtncagat ctggaaggct ttgttatata aacatttttt taatgtttat tggcaagaat 180
 acttttctaa gagaaacatc agtgagctgg tttccattta agctgaatga agccacaatg 240
 tacctcangt ataaggatta actggccttt ttccagttgc actctaatta caattttaga 300
 atgatgttcn gaggccacct gtcaaatagca ttc 333

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<210> 34
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 <212> PRT
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<400> 34
 Gln Ala Cys Gln Gly
 1 5

<210> 35
 <211> 5

<212> PRT
<213> Homo sapiens

<400> 35
Gln Asn Tyr Val Val
1 5